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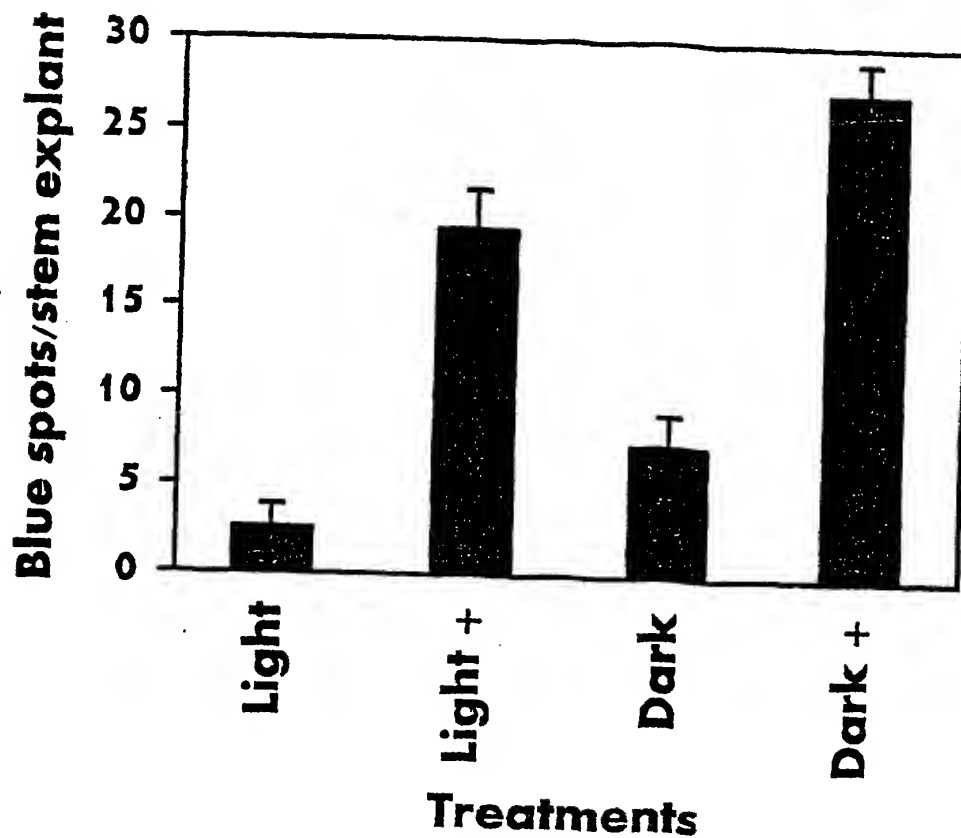


Fig. 1

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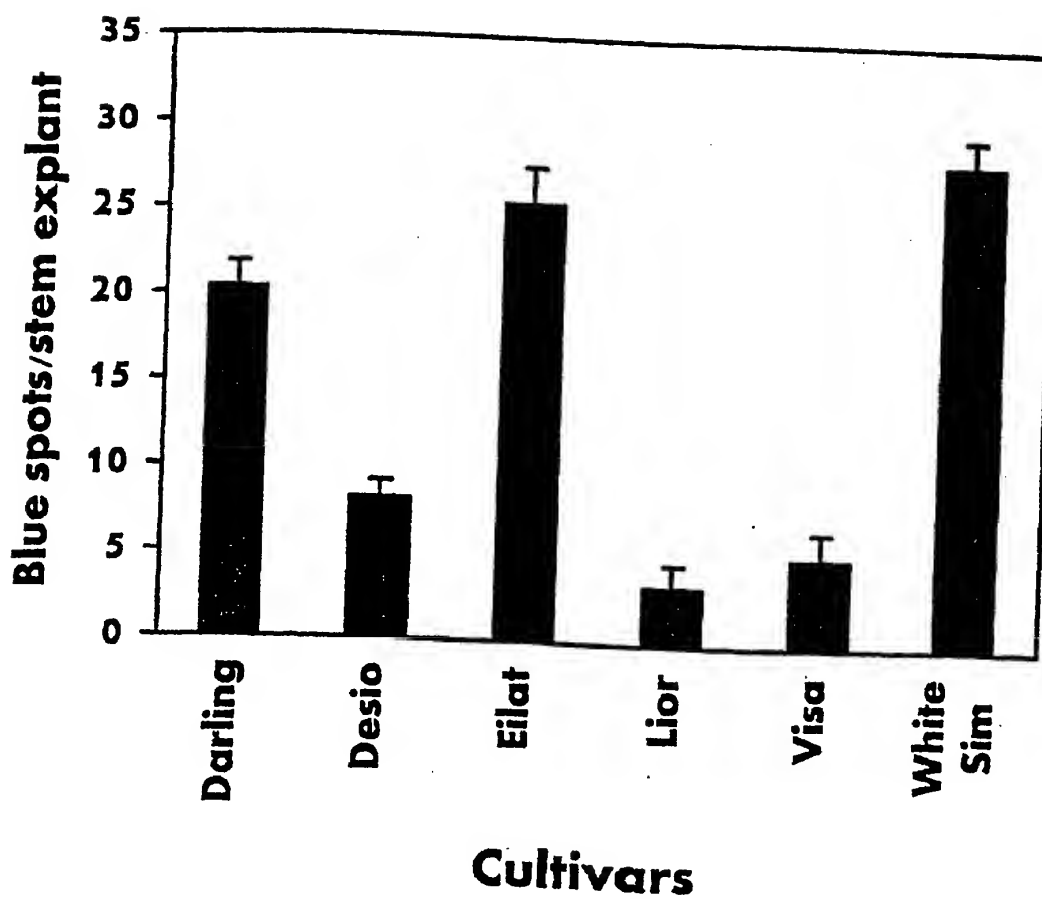


Fig. 2

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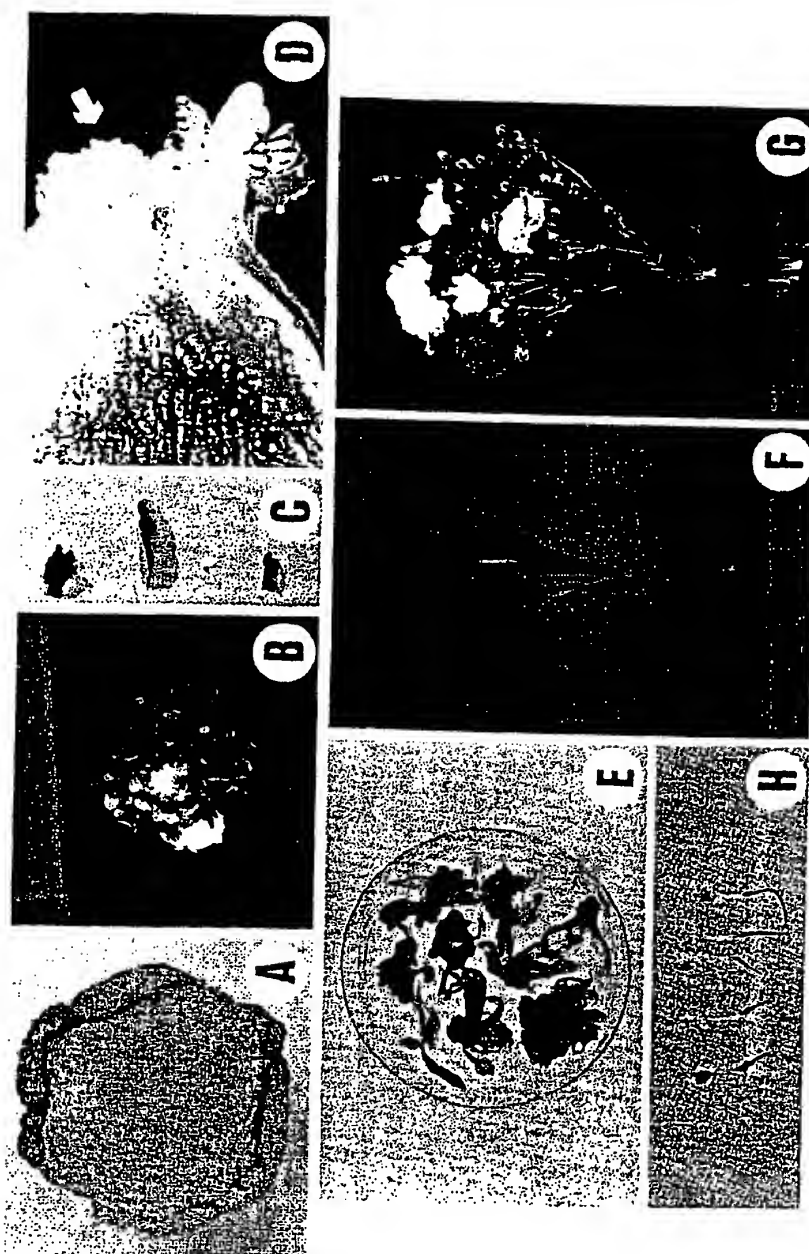


Fig. 3

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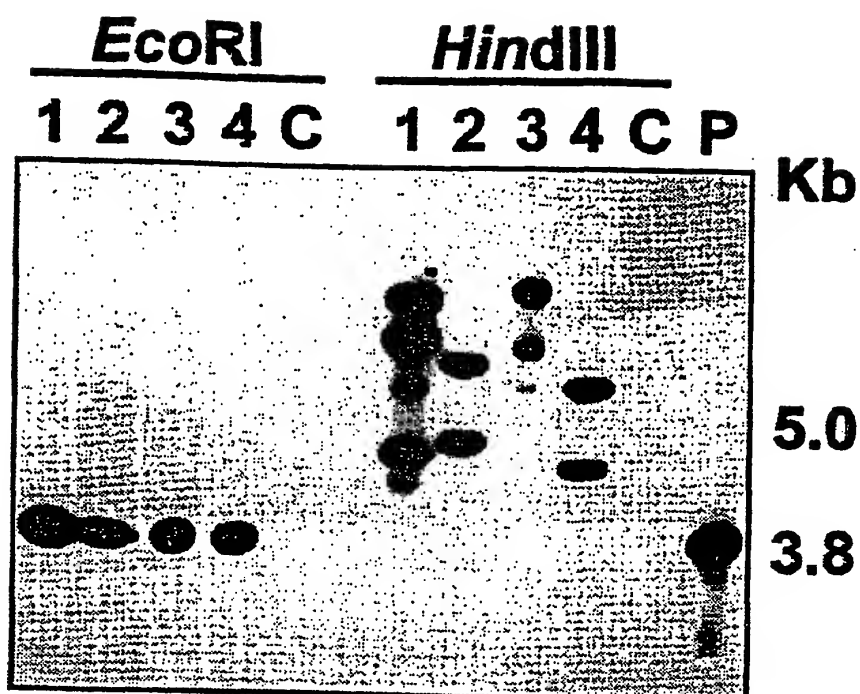


Fig. 4

206270" 94747E60

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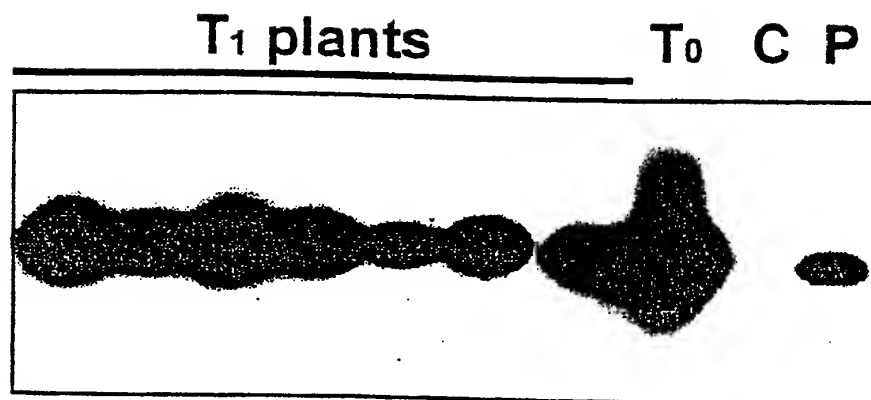


Fig. 5

800bp

206270" 94T4T650

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205210" 9444660

1 ATGGCTGAAG ACGACCTGTG TTCTCTCTTT TTCAAGCTCA AAGTGGAGGA TGTGACAAGC  
61 ACGGATGAGC TAGCTAGACA CATGAAGAAC GCCTCAAATG AGCGTAAACC CTTGATCGAG  
121 CCGGGTGAGA ATCAATCGAT GGATATTGAC GAAGAAGGAG GGTCGGTGGG CCACGGGCTG  
181 CTGTACCTCT ACGTCGACTG CCCGACGATG ATGCTCTGCT TCTATGGAGG GTCCCTGCCT  
241 TACAATTGGA TGAAGGGCGC ACTCCTCACC AACCTTCCCC CGTACCAGCA TGATGTGACT  
301 CTCGATGAGG TCAATAGAGG GCTCAGGCAA GCATCAGGTT TTTTCGGTTA CGCGGATCCT  
361 ATGCGGAGCG CCTACTTCGC TGCATTTTCT TTCCCTGGGC GTGTCAATCA GCTGAATGAG  
421 CAGATGGAGC TAACTTCGAC AAAGGGAAG TGCTGACAT TCGACCTCTA TGCCAGCACC  
481 CAGCTTAGGT TCGAACCTGG TGAGTTGGTG AGGCATGGCG AGTCAAGTT TGCAATCGGC  
541 TAATGGTTAG TCGATGGGCT GACGAGTTTG ATGTCAGGAG AAGCTGAGTG TGTCACTTGT  
601 TTCCCTTTAA GAAGTATTAA TGTAATAAAA ATCAAGATCT GGTTTAATA CTGGATACTT  
661 GATTTCATCG CGCTTTTTTT GAATAAATGT TTGTTGTCTT GACTTTAAGA TATCCTTTGA  
721 AATTGCGGTT ATTCGTATTT CGCTTTTGGT TATTTCCAAA AGACTTTGCT CAGTAAGATC  
781 AAACGTTTGT ATTCTCCGG GCCACAATAT TTGACCTATA TGCCTGGCC CACGCGCCGC  
841 AATAGATGAA AATTGCCAAA ATTAGCTATC GGTCTTCTGA AAAGAAGGGC CGACATGTTT

Fig. 6

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206210" SHHTE60

901 TCATAGACCA TGCAAAGTCA TACTACCTGA AACTGATAAA TAACGACAAA GAAAGTAGCC  
961 TATTAAAAG TCGCTATAGC ATGAATT

Fig. 6 (cont.)

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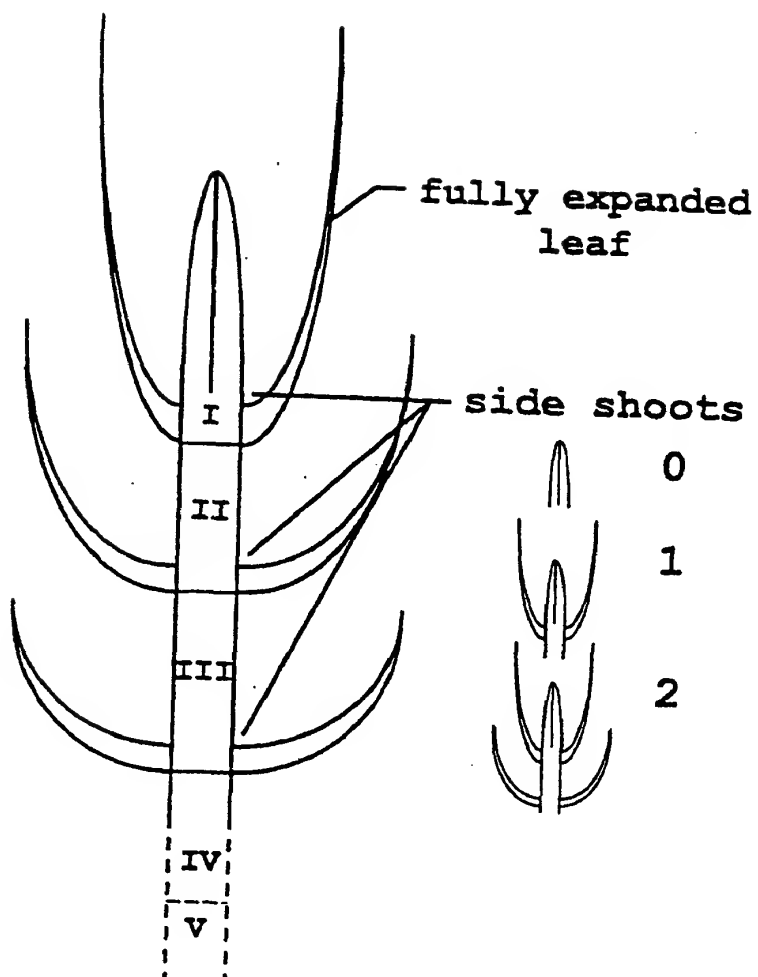


Fig. 7



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206270" 94747660

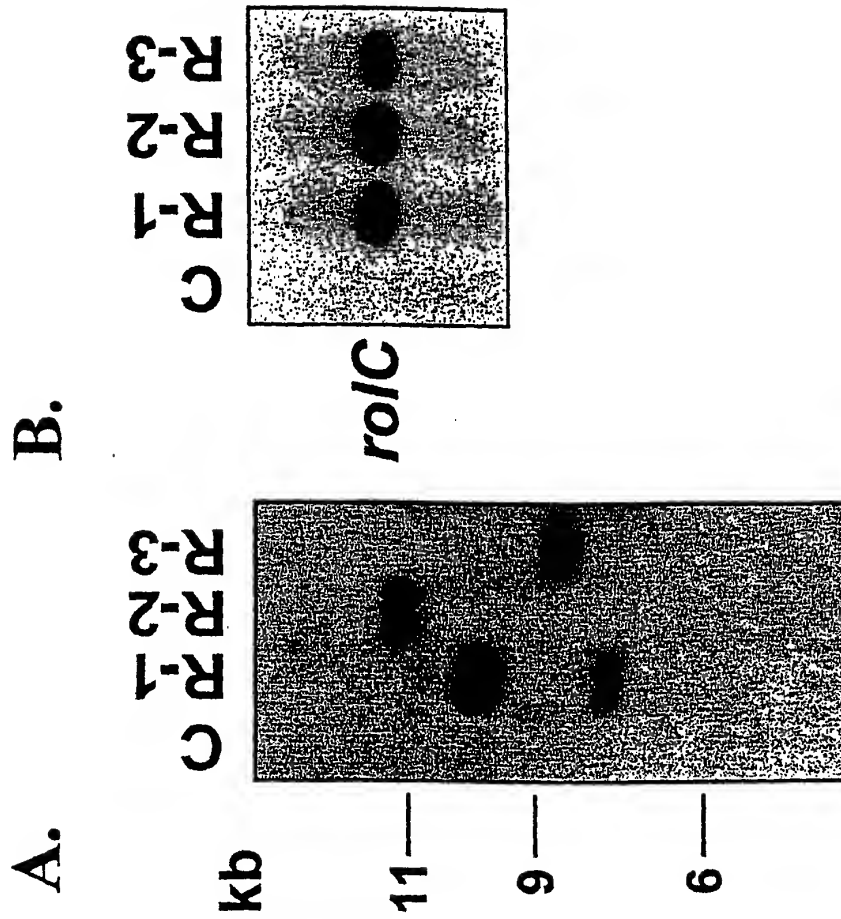


Fig. 8

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206270" SHHT660

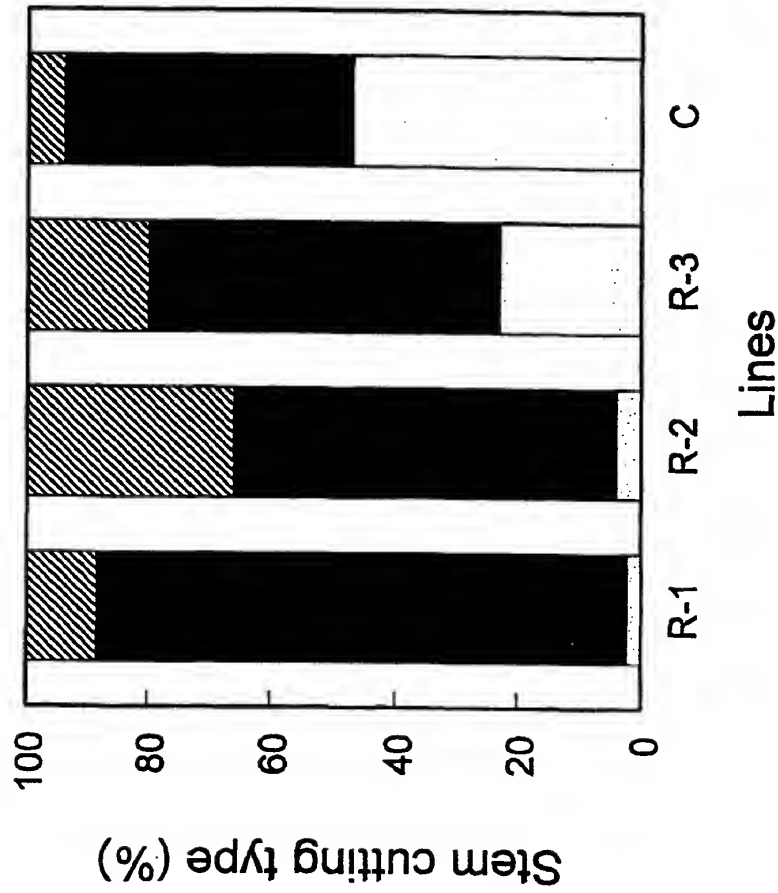


Fig. 9

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206210" 9444650

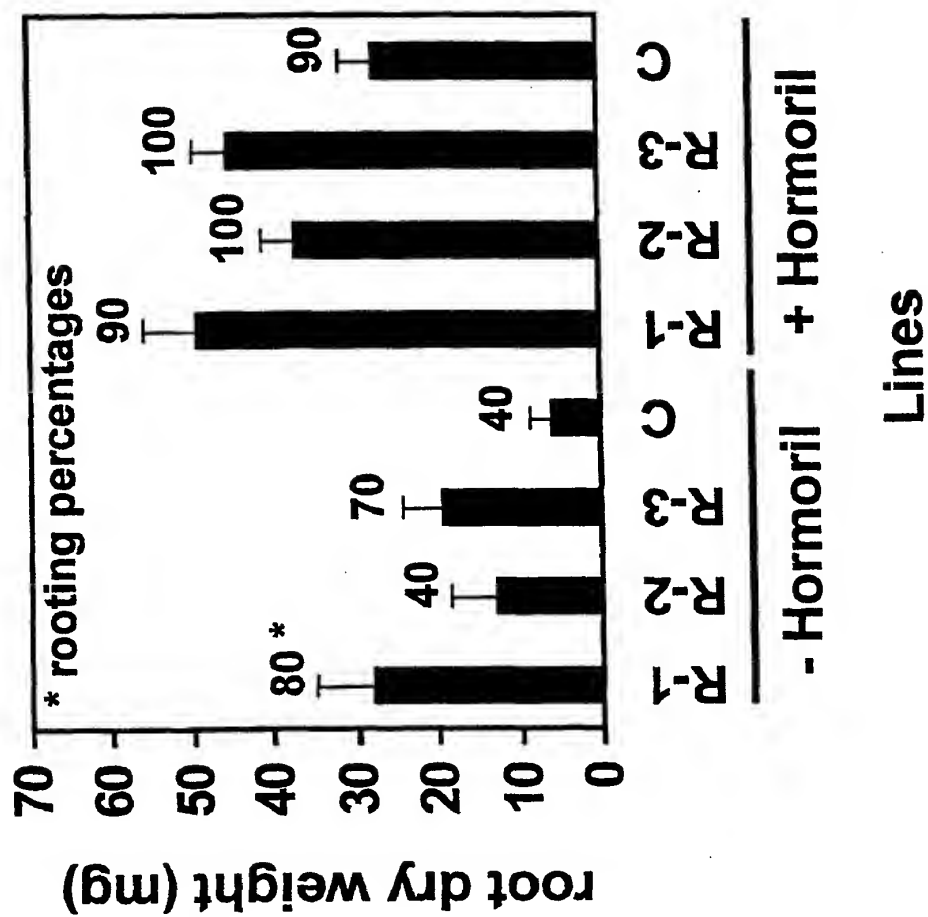


Fig. 10

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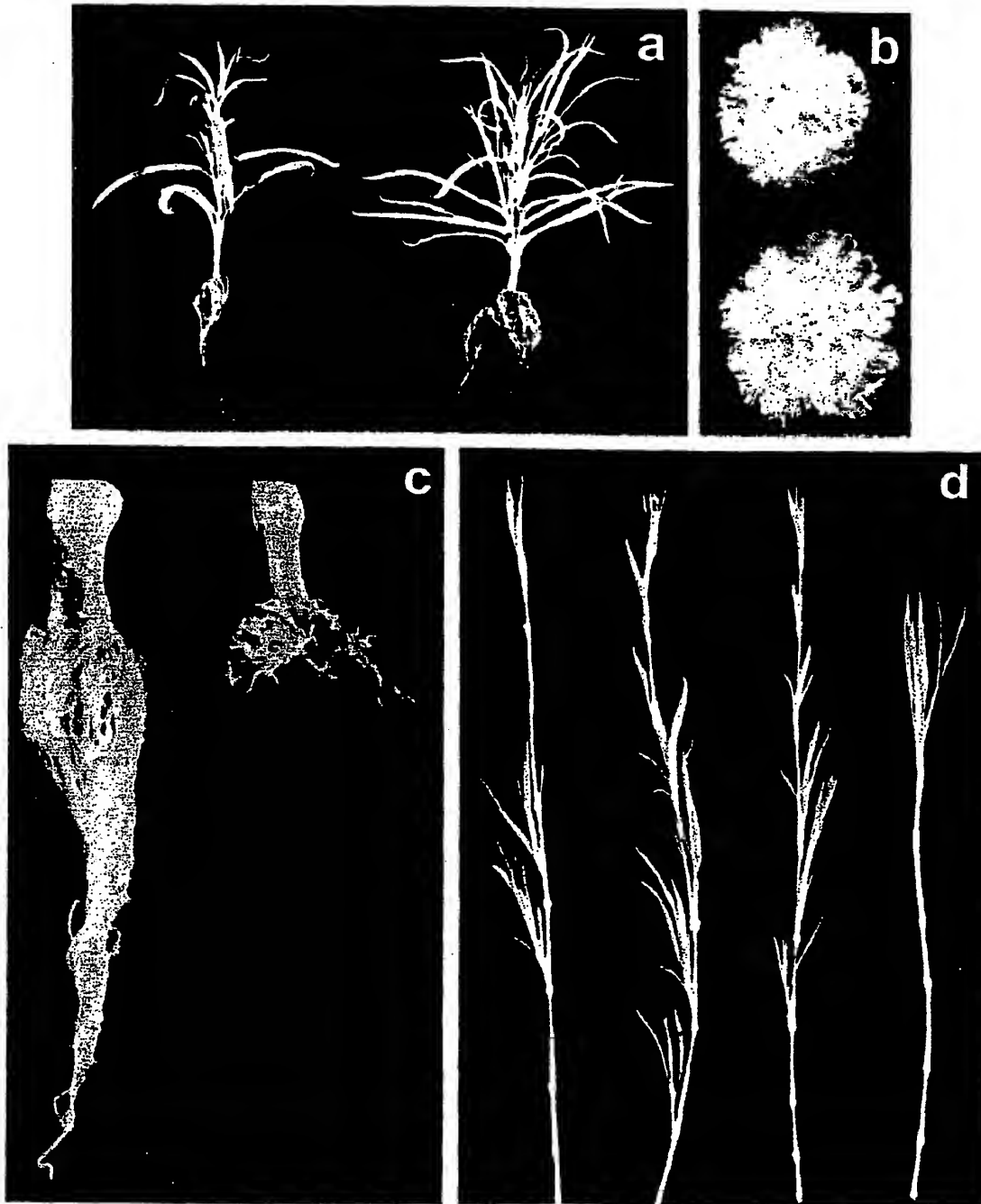


Fig. 11

206270-914146

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09914146-012902

1 ACTATATCTT AAATATTCAC AACATTATAA CATAAGCTTC AAAATAACAT  
51 TATTCCGATA TTTACGTAAT ATAATACGTA TCATATTAGG GTACATTCAT  
101 TTTATCAACT ACGACTGCAT ATTGTTAGAC AGTCTCATAT ATACGCATAA  
151 AAAATGGTCG CTGAAAAACC CAAAACGCTC ACTTCACTAG AAGGGGACGA  
201 TAAATTGAAC TCGAATTTTG TTAGGGACGA GGATGAACGT CCGAAAGTGG  
251 CGTATAATGA GTTTAGCAAT GATATTCCGG TGATATCTCT TGCTGGTATA  
301 GATGGTGAAA AAAGGGGTGA AATATGTCGG AAGATTGTTG AGGCGTGTGA  
351 AGATTGGGGG ATTTTTCAAG TGGTTGATCA CGGTGTGGT GACGATCTTA  
401 TTGCTGATAT GACTCGGTTG GCTCGTGAAT TTTTCGCTCT CCCGGCAGAA  
451 GAGAAGCTCC GATTTGATAT GTCTGGTGGT AAAAAGGGCG GTTTTATCGT  
501 GTCGAGTCAT CTTCAGGTTCAATCAACAGG GAGAAGTAGT GCAGGACTGG  
551 AGGGAAATCGTGACGTATTT CTCATACCCG ACGAACTCAA GGGACTACAC  
601 AAGATGGCCAGACAAACCAG AGGGTTGGAT AAAGGTCACA GAGGAATACA  
651 GCAACAAGTTAATGACCTTA GCATGTACAC TTTTAGGTGT ACTTTCTGAA  
701 GCCATGGGTTTAGAATTAGA GGCACCTACT AAAGCTTGTG TTGATATGGA  
751 CCAAAGATTGTGGTTAATT ACTACCCTAA GTGCCCTCAA CCTGACCTTA  
801 CTTTAGGGCTCAAGAGGCAC ACCGACCCCG GGACTATAAC CCTCCTCCTT  
851 CAGGACCAAGTCGGCGGTCT TCAGGCCACT CGTGACGGTG GTAAAACTTG  
901 GATTACCGTG CAGCCGGTTC CCGGTGCCTT CGTTGTAAAC CTTGGTGATC  
951 ATGGTCATGTTGCGCGAAAA ATGGCCAAAG ACCTTGAGAT CGCCCGTCAT  
1001 AAGAGGCTTG CTAAAGAGGA AATGCCTTTT AAAGAGTTGG ACGAGGCCAA  
1051 GTTTGAGTCC AAATCTATTG ACCAAATACT TGCTTAGATG GGCTTGTTT  
1101 GGTTTCATTA TATTAAATTT ATTATTATTA TTATTTATTG CATTTGATAT  
1151 GATATGATTG GAAATAAAAG AGAGATTGTT TGTGATAATT TGTGTGATTA  
1201 TTATATCACT AAGTTATGGC TTTAATTTGT GGTATGTTGG GAATTATATA  
1251 TTTAGTTTTG TGTGAAGAAT ATATGATTTA AAGTTAAAAA AAAAAATGAT  
1301 TTGTTATATGATTTACTTGT AAGGTTATAA GGTATATTTT ATTGTTGAG  
1351 TTTGCGTATA

Fig. 12

206210" 94441660

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1 CCAAGCCCAT CTAAGCAAGT ATTGGTCAA TAGATTGGGA CTCAAACTTG GCCTCGTCCA  
61 ACTCTTTAAA AGGCATTTCC TCTTTAGCAA GCCTCTTATG ACGGCGGATC TCAAGTCTT  
121 TGGCCATTTT TCGCCGAACA TGACCATGAT CACCAAGGTT AACAAACGAAG GCACCCGGAA  
181 CCGGCTGCAC GGTAATCCAA GTTTACCAC CGTCACGAGT GGCCTGAAGA CCGCCGACTT  
241 GGTCCTGAAG GAGGAGGGTT ATAGTCCCGG GGTCGGGTGTG CCTCTTGAGC CCTAAAGTAA  
301 GGTCAGGTG AGGGCACTTA GGTAGTAAT TAACCACAAT CTTTGGTCC ATATCAACAC  
361 AAGCTTTAGT AAGTGCCCTCT AATTCTAAAC CCATGGCTTC AGAAAGTACA CCTAAAGTG  
421 TACATGCTAA GGTCAATTAA TGTGTGCTGT ATTCTCTGT GACCTTTATC CAACCTCTG  
481 GTTTGTCTGG CCATCTTGTG TAGTCCCTTG AGTTCGTGG GTATGAGAAA TACGTCAACGA  
541 TTTCCCTCCA GTCCTGCACT ACTTCTCCCT GTTGATTGAA CCTGAAGATG ACTCGACACG  
601 ATAAACCGC CCTTTTACC ACCAGACATA TCAAATCGGA GCTTCTCTTC TGCCGGGAGA  
661 GCGAAAAATT CACGAGCCAA CCGAGTCATA TCAGCAATAA GATCGTCACC AACACCGTGA  
721 TCAACCACTT GAAAAATCCC CCAATCTTCA CAGGCCTCAA CAATCTTCCG ACATATTTCA  
781 CCCCTTTTTT CACCATCTAT ACCAGCAAGA GATATCACCG GAATATCAAT GCTAAACTCA  
841 TTATACGCCA CTTTCGGACG TTCAATCCTCG TCCCTAACAA AATTCGAGTT CAATTTATCG  
901 TCCCTTCTA GTGAAGTGAG CGTTTGGG

Fig. 13

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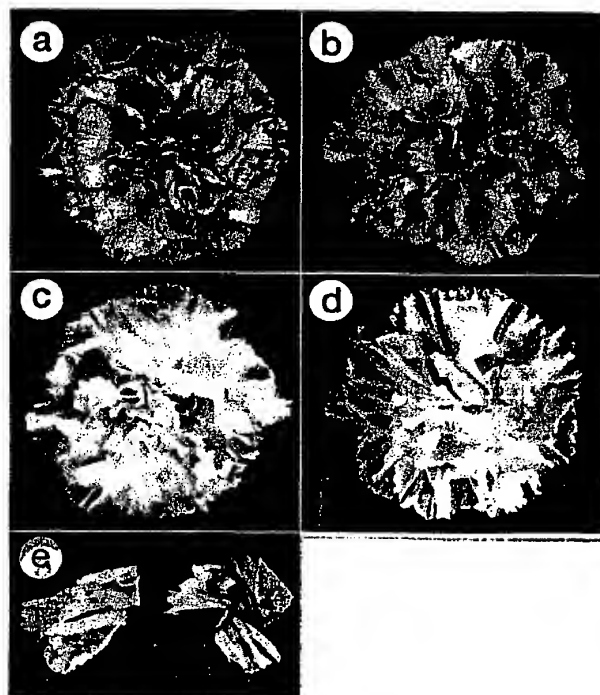


Fig. 14

206210" 94T4T660

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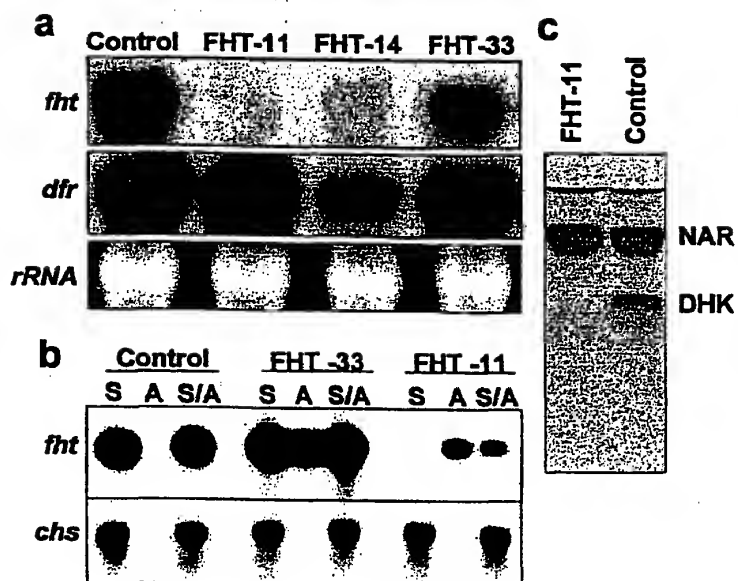


Fig. 15

206270-94747660



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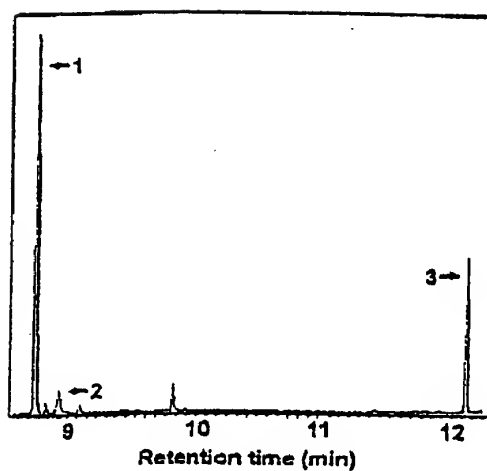


Fig. 16

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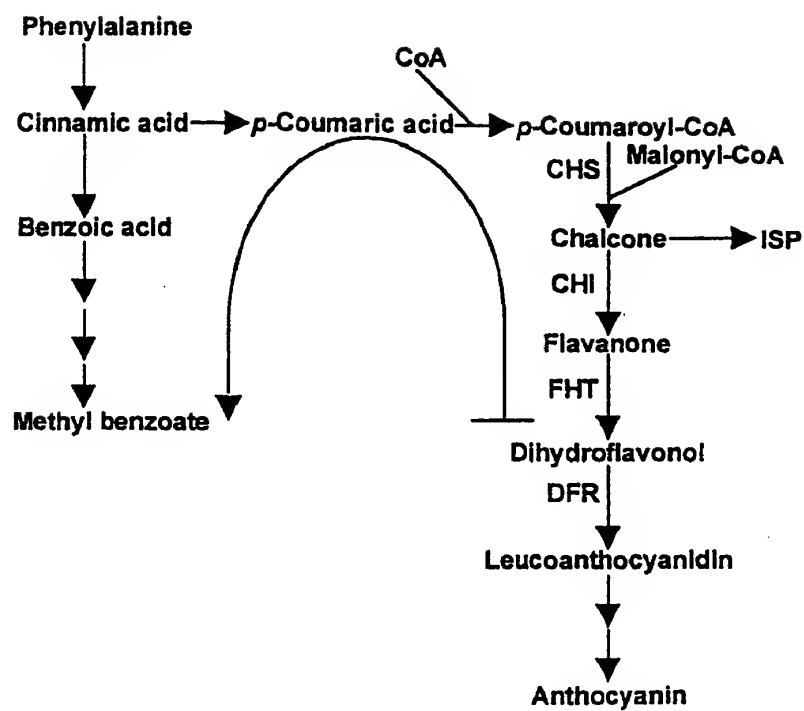


Fig. 17